RAW SEQUENCE LISTING ERROR REPORT
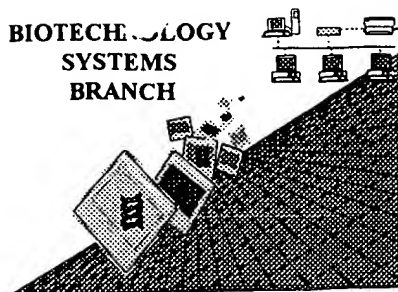
BIOTECHNOLOGY
SYSTEMS
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/756,301_

Source: _OIPE_

Date Processed by STIC: _1/25/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 09/756,30/ |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

```
RAW SEQUENCE LISTING              DATE: 01/25/2001
PATENT APPLICATION: US/09/756,301 TIME: 10:37:58

Input Set : A:\0975.1005-008SEQLIST.txt
Output Set: N:\CRF3\01252001\I756301.raw
```

Does Not Comply
Corrected Diskette Needed

see pp 1-5

Suggestion: Consult new Sequence Rules.

```
 4 <110> APPLICANT: Junming Le
 5          Jan Vilcek
 6          Peter Daddona
 7          John Ghrayeb
 8          David M. Knight
 9          Scott Siegel
11 <120> TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
12          Human Tumor Necrosis Factor
15 <130> FILE REFERENCE: 0975.1005-008
17 <140> CURRENT APPLICATION NUMBER: US/09/756,301
17 <141> CURRENT FILING DATE: 2001-01-08
17 <150> PRIOR APPLICATION NUMBER: U.S. 09/133,119
18 <151> PRIOR FILING DATE: 1998-08-12
20 <150> PRIOR APPLICATION NUMBER: U.S. 08/570,674
21 <151> PRIOR FILING DATE: 1995-12-11
23 <150> PRIOR APPLICATION NUMBER: U.S. 08/324,799
24 <151> PRIOR FILING DATE: 1994-10-18
26 <150> PRIOR APPLICATION NUMBER: U.S. 08/192,102
27 <151> PRIOR FILING DATE: 1994-02-04
29 <150> PRIOR APPLICATION NUMBER: U.S. 08/192,861
30 <151> PRIOR FILING DATE: 1994-02-04
32 <150> PRIOR APPLICATION NUMBER: U.S. 08/192,093
33 <151> PRIOR FILING DATE: 1994-02-04
35 <150> PRIOR APPLICATION NUMBER: U.S. 08/010,406
36 <151> PRIOR FILING DATE: 1993-01-29
38 <150> PRIOR APPLICATION NUMBER: U.S. 08/013,413
39 <151> PRIOR FILING DATE: 1993-02-02
41 <150> PRIOR APPLICATION NUMBER: U.S. 07/943,852
42 <151> PRIOR FILING DATE: 1992-09-11
44 <150> PRIOR APPLICATION NUMBER: U.S. 07/853,606
45 <151> PRIOR FILING DATE: 1992-03-18
47 <150> PRIOR APPLICATION NUMBER: U.S. 07/670,827
48 <151> PRIOR FILING DATE: 1991-03-18
50 <160> NUMBER OF SEQ ID NOS: 19
52 <170> SOFTWARE: FastSEQ for Windows Version 4.0
54 <210> SEQ ID NO: 1
55 <211> LENGTH: 157
56 <212> TYPE: PRT
57 <213> ORGANISM: Peptide   invalid response
59 <400> SEQUENCE: 1
60 Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
61  1               5                  10                  15
62 Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
63              20                  25                  30
64 Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
65              35                  40                  45
66 Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
```

Per 1.823 of new Sequence Rules, the only valid responses for <213> are: Unknown, Artificial Sequence, or Scientific name (Genus/species) (see circled portion of item 12 on Err Sheet)

```
        RAW SEQUENCE LISTING              DATE: 01/25/2001
        PATENT APPLICATION:  US/09/756,301   TIME: 10:37:58

        Input Set : A:\0975.1005-008SEQLIST.txt
        Output Set: N:\CRF3\01252001\I756301.raw

67      50                      55                      60
68  Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
69  65                      70                      75                      80
70  Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
71                      85                      90                      95
72  Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
73                      100                     105                     110
74  Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
75          115                     120                     125
76  Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
77      130                     135                     140
78  Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
79  145                     150                     155
82  <210> SEQ ID NO: 2
83  <211> LENGTH: 321
84  <212> TYPE: DNA
85  <213> ORGANISM: CDNA
87  <220> FEATURE:
88  <221> NAME/KEY: CDS
89  <222> LOCATION: (0)..(321)
91  <400> SEQUENCE: 2
92  gac atc ttg ctg act cag tct cca gcc atc ctg tct gtg agt cca gga   48
93  Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
94  1                       5                       10                      15
96  gaa aga gtc agt ttc tcc tgc agg gcc agt cag ttc gtt ggc tca agc   96
97  Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
98                      20                      25                      30
100 atc cac tgg tat cag caa aga aca aat ggt tct cca agg ctt ctc ata   144
101 Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
102         35                      40                      45
104 aag tat gct tct gag tct atg tct ggg atc cct tcc agg ttt agt ggc   192
105 Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
106         50                      55                      60
108 agt gga tca ggg aca gat ttt act ctt agc atc aac act gtg gag tct   240
109 Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
110 65                      70                      75                      80
112 gaa gat att gca gat tat tac tgt caa caa agt cat agc tgg cca ttc   288
113 Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
114                     85                      90                      95
116 acg ttc ggc tcg ggg aca aat ttg gaa gta aaa   321
117 Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
118         100                     105
121 <210> SEQ ID NO: 3
122 <211> LENGTH: 107
123 <212> TYPE: PRT
124 <213> ORGANISM: Protein
126 <400> SEQUENCE: 3
127 Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
128 1                       5                       10                      15
```

(handwritten annotations) → see previous page regarding valid <213> responses

(1) — first base begins at location 1

same ones as above

```
                      RAW SEQUENCE LISTING            DATE: 01/25/2001
                      PATENT APPLICATION:  US/09/756,301   TIME: 10:37:58

                      Input Set : A:\0975.1005-008SEQLIST.txt
                      Output Set: N:\CRF3\01252001\I756301.raw

      129 Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
      130             20                  25              30
      131 Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
      132         35                  40              45
      133 Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
      134     50                  55              60
      135 Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
      136 65              70                  75                  80
      137 Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
      138             85                  90                  95
      139 Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
      140             100                 105
      143 <210> SEQ ID NO: 4
      144 <211> LENGTH: 357
      145 <212> TYPE: DNA
      146 <213> ORGANISM: CDNA
      148 <220> FEATURE:
      149 <221> NAME/KEY: CDS
W-->  150 <222> LOCATION: (0)..(357)
      152 <400> SEQUENCE:
      153 gaa gtg aag ctt gag gag tct gga gga ggc ttg gtg caa cct gga gga   48
      154 Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
      155 1               5                   10                  15
      157 tcc atg aaa ctc tcc tgt gtt gcc tct gga ttc att ttc agt aac cac   96
      158 Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
      159             20                  25                  30
      161 tgg atg aac tgg gtc cgc cag tct cca gag aag ggg ctt gag tgg gtt   144
      162 Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
      163         35                  40                  45
      165 gct gaa att aga tca aaa tct att aat tct gca aca cat tat gcg gag   192
      166 Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
      167     50                  55                  60
      169 tct gtg aaa ggg agg ttc acc atc tca aga gat gat tcc aaa agt gct   240
      170 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala
      171 65              70                  75                  80
      173 gtc tac ctg caa atg acc gac tta aga act gaa gac act ggc gtt tat   288
      174 Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr
      175             85                  90                  95
      177 tac tgt tcc agg aat tac tac ggt agt acc tac gac tac tgg ggc caa   336
      178 Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln
      179             100                 105                 110
      181 ggc acc act ctc aca gtc tcc                                      357
      182 Gly Thr Thr Leu Thr Val Ser
      183             115
      186 <210> SEQ ID NO: 5
      187 <211> LENGTH: 119
      188 <212> TYPE: PRT
      189 <213> ORGANISM: Protein
      191 <400> SEQUENCE:
```

```
192 Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
193 1               5              10              15
194 Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
195             20              25              30
196 Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
197             35              40      .       45
198 Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
199     50              55              60
200 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala
201 65              70              75              80
202 Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr
203             85              90              95
204 Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln
205             100             105             110
206 Gly Thr Thr Leu Thr Val Ser
207             115
210 <210> SEQ ID NO: 6
211 <211> LENGTH: 8
212 <212> TYPE: PRT
213 <213> ORGANISM: Protein
215 <400> SEQUENCE: 6
216 Gly Thr Leu Val Thr Val Ser Ser
217 1               5
220 <210> SEQ ID NO: 7
221 <211> LENGTH: 7
222 <212> TYPE: PRT
223 <213> ORGANISM: Protein
225 <400> SEQUENCE: 7
226 Gly Thr Lys Leu Glu Ile Lys
227 1               5
230 <210> SEQ ID NO: 8
231 <211> LENGTH: 20
232 <212> TYPE: DNA
233 <213> ORGANISM: cDNA
235 <400> SEQUENCE: 8
236 cctggatacc tgtgaaaaga                              20
238 <210> SEQ ID NO: 9
239 <211> LENGTH: 27
240 <212> TYPE: DNA
241 <213> ORGANISM: cDNA
243 <400> SEQUENCE: 9
244 cctggtacct tagtcaccgt ctcctca                      27
246 <210> SEQ ID NO: 10
247 <211> LENGTH: 27
248 <212> TYPE: DNA
249 <213> ORGANISM: cDNA
251 <400> SEQUENCE: 10
252 aatagatatc tccttcaaca cctgcaa                      27
254 <210> SEQ ID NO: 11
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RAW SEQUENCE LISTING   DATE: 01/25/2001
PATENT APPLICATION: US/09/756,301   TIME: 10:37:58

Input Set : A:\0975.1005-008SEQLIST.txt
Output Set: N:\CRF3\01252001\I756301.raw

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255 <211> LENGTH: 21
256 <212> TYPE: DNA
257 <213> ORGANISM: cDNA
259 <400> SEQUENCE: 11
260 atcgggacaa agttggaaat a                    21
262 <210> SEQ ID NO: 12
263 <211> LENGTH: 16
264 <212> TYPE: DNA
265 <213> ORGANISM: cDNA
267 <400> SEQUENCE: 12
268 ggcggtctgg taccgg                          16
270 <210> SEQ ID NO: 13
271 <211> LENGTH: 19
272 <212> TYPE: DNA
273 <213> ORGANISM: cDNA
275 <400> SEQUENCE: 13
276 gtcaacaaca tagtcatca                       19
278 <210> SEQ ID NO: 14
279 <211> LENGTH: 23
280 <212> TYPE: DNA
281 <213> ORGANISM: cDNA
283 <400> SEQUENCE: 14
284 cacaggtgtg tccccaagga aaa                   23
286 <210> SEQ ID NO: 15
287 <211> LENGTH: 18
288 <212> TYPE: DNA
289 <213> ORGANISM: cDNA
291 <400> SEQUENCE: 15
292 aatctggggt aggcacaa                         18
294 <210> SEQ ID NO: 16
295 <211> LENGTH: 17
296 <212> TYPE: DNA
297 <213> ORGANISM: cDNA
299 <400> SEQUENCE: 16
300 agtgtgtgtc cccaagg                          17
302 <210> SEQ ID NO: 17
303 <211> LENGTH: 24
304 <212> TYPE: DNA
305 <213> ORGANISM: cDNA
307 <400> SEQUENCE: 17
308 cacagctgcc cgcccaggtg gcat                  24
310 <210> SEQ ID NO: 18
311 <211> LENGTH: 17
312 <212> TYPE: DNA
313 <213> ORGANISM: cDNA
315 <400> SEQUENCE: 18
316 gtcgccagtg ctccctt                          17
318 <210> SEQ ID NO: 19
319 <211> LENGTH: 20
```

Please correct these errors in seq. 19, too.

VERIFICATION SUMMARY   DATE: 01/25/2001
PATENT APPLICATION: US/09/756,301   TIME: 10:37:59

Input Set : A:\0975.1005-008SEQLIST.txt
Output Set: N:\CRF3\01252001\I756301.raw

L:17 M:270 C: Current Application Number differs, Replaced Current Application No
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:89 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:2, CDS LOCATION: (0)...(321)
L:150 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:4, CDS LOCATION: (0)...(357)